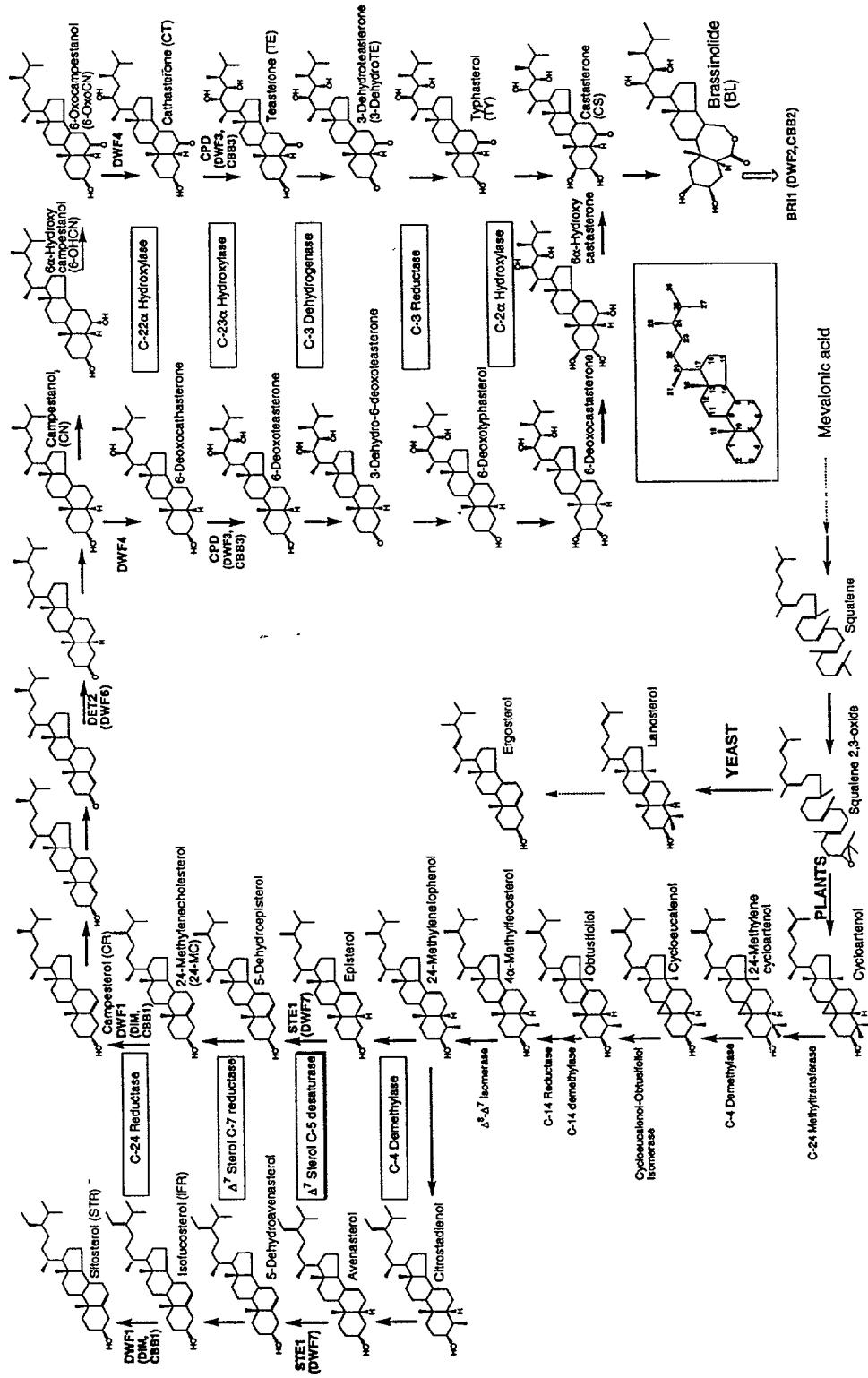


Sterol-Specific Biosynthetic Pathway



BR-Specific Biosynthetic Pathway

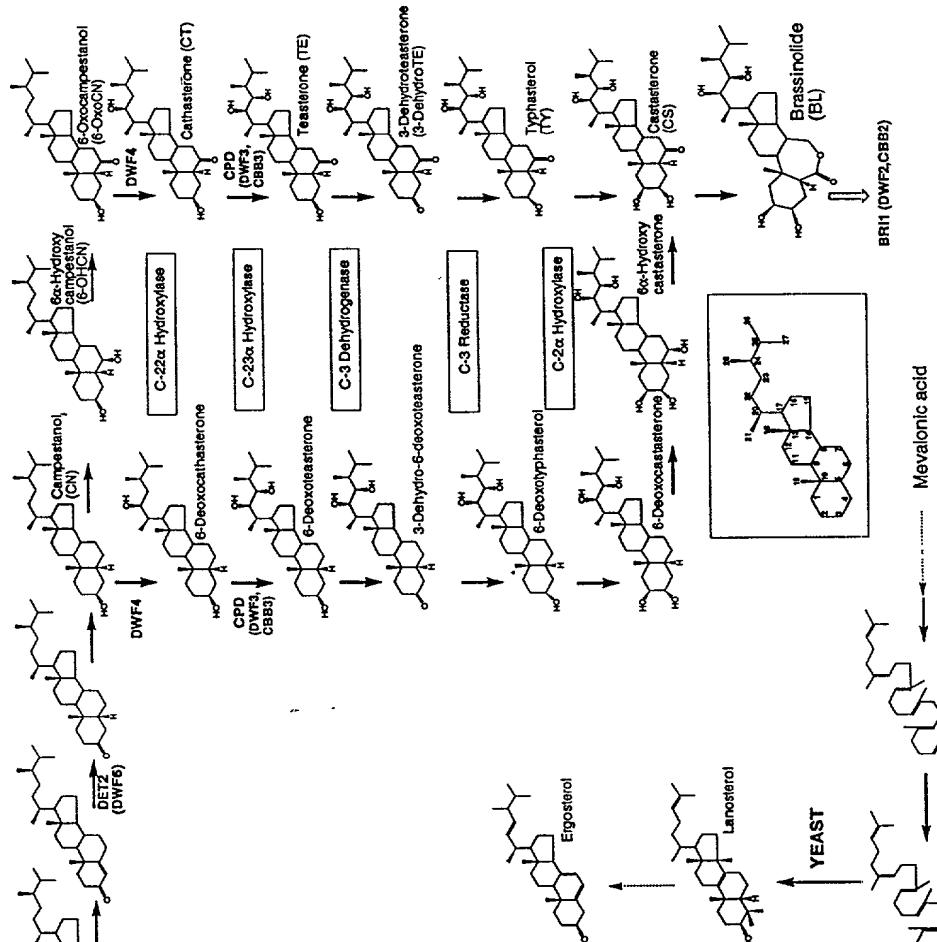


FIG. 1

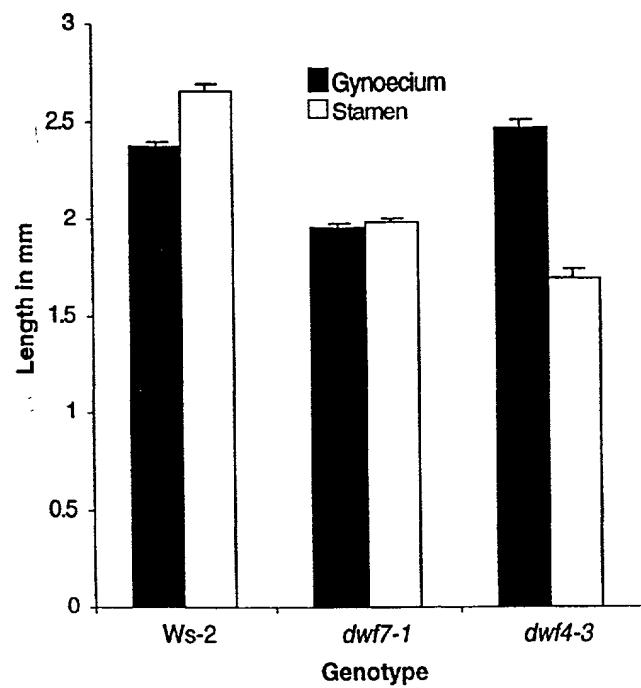


FIG. 2

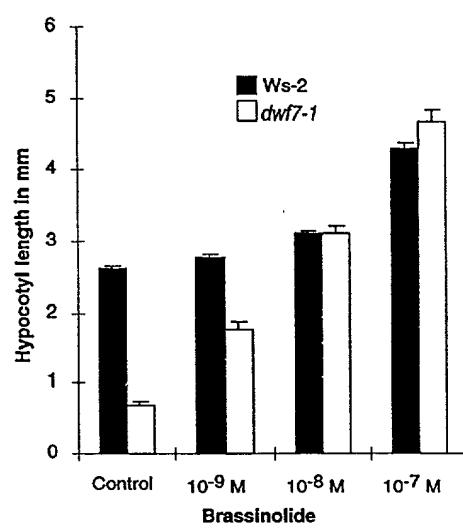


FIG. 3

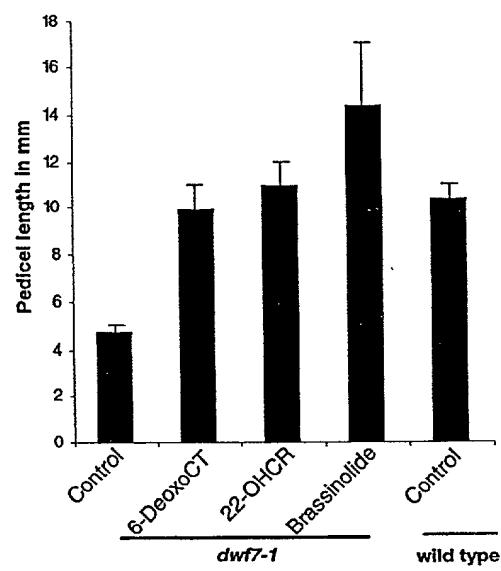


FIG. 4

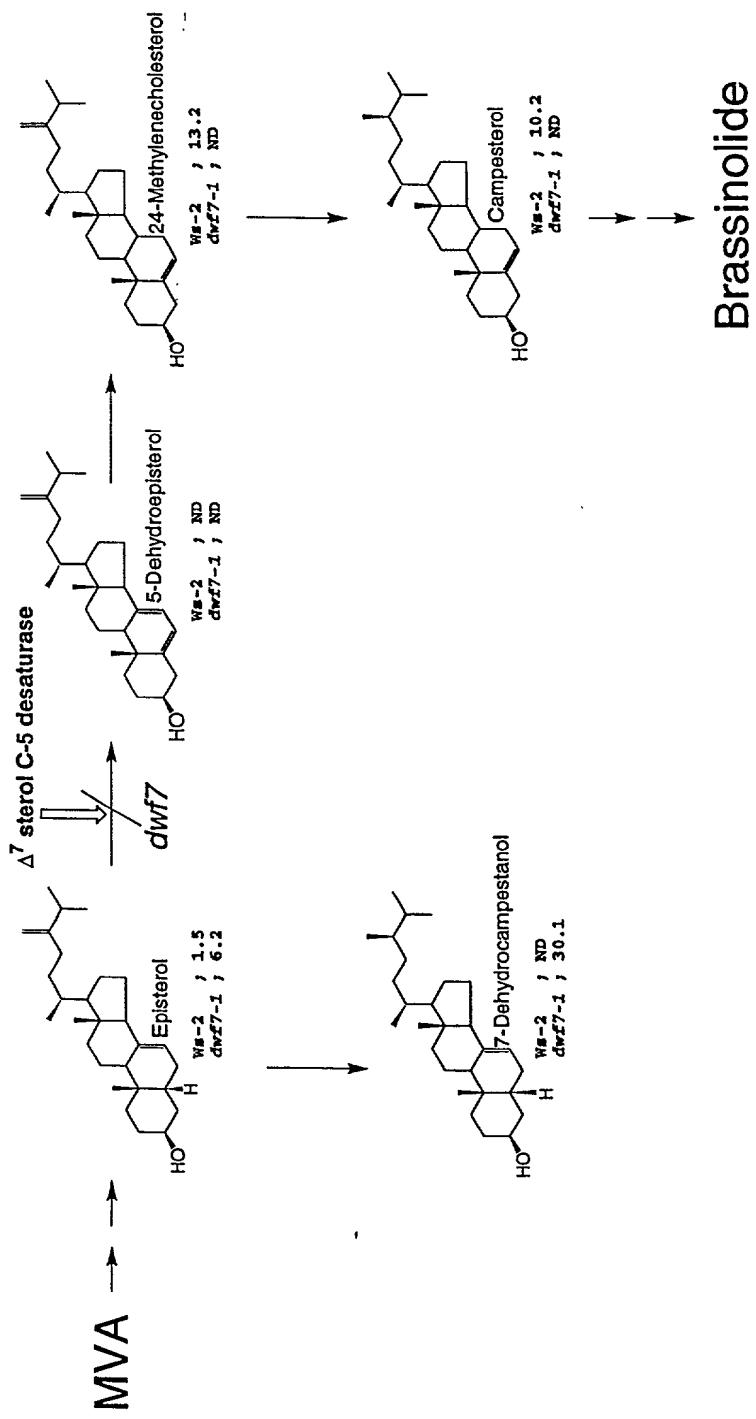


FIG. 5

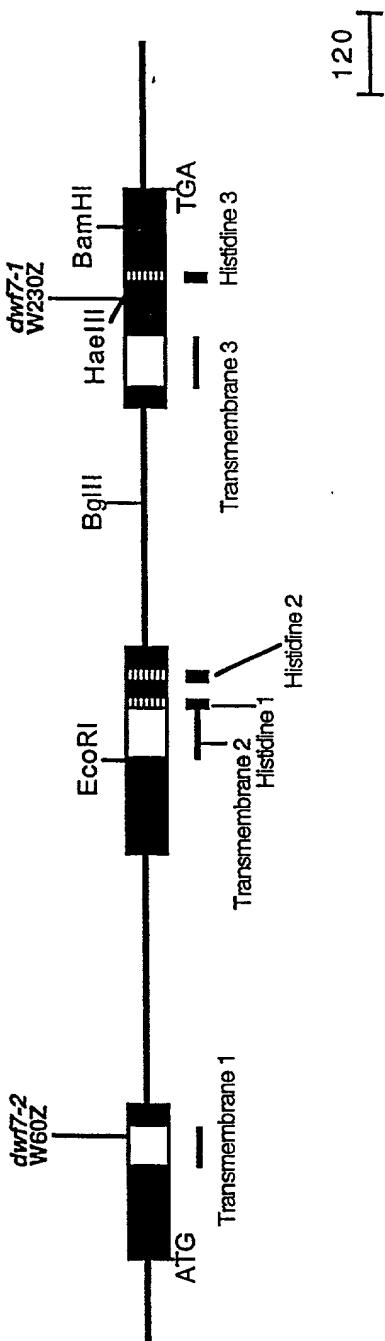


FIG. 6

C. glabrata 1 10 20 30 40
S. cerevisiae MDLVLETLDHYLFDDVYAKAIPVQLORGIDDSLVLNALSLNKIVSNSTL
S. pombe MDLVLEVADHYVLDDLAKVLPASLAANIPVKWQKLGLNSGFSNSTL
DWFT7-STE1 MDVVLQYADKRYVFDTFYQKIL---AESFDSS-SSFA-NTAVFNSTL
Consensus mdlvle-adhyvfdd-yaki-p-lla-ids---ilin-vsnst-i

50 60 70 80 90 100 110
HETL LSITNSLKRVNKDGVYGLTPFLFOF-TEKTY-ASLLPRNNLIR---EFFSLWAV
QETL LNSKNAVKMECCR-FYQOVPFLEDM-STTSF-ASLLPRRSSLRL---EFLSLWV
TTLGL ---AEKVN---FAIT---SGLLDRNNVWR---QFTSFLI
--- ---MAADNAYLMOFVDETSFVYNRIVLSLHRLPAN-LWEPLPHEQTLWLR
-eti ---n---k-vn---y-g-pfifdf-tetsf---sllprnnlwr---eFisiwii

120 130 140 150 160 170
VIVM FGLLLILYLTASL-SYVVFVDFR-TIFNHPK-YLKNQMYLEIKLAVSAIPTMSLL-T
VTI FGLLLILYLTASL-SYVVFVDFK-SIFNHPD-YLKNQMAIMEIKLAVSAIPWMSML-T
TWL MGTLSYFLSASE-AMYVYDFEEARHPK-FLKNOEHLMLVALKNLPGMALL-T
NYLAGT LLYFIISGF-WCFYIYLLKINVYL-PKDAIPTIK-AMRLQMFVAKAMPWYTLPLP
VtiifG-LTY-i-asi-sy-1-1d---ifnhPk---yIKnqm-leik-Av-aiPwmsmLL-T

Transmembrane I dwf7-2 (W to Z)

180 190 200 210 220 230
VPWF MLELNGYSKLYYDWDWEHHLGRKLLIEYATEIIFTDCGJYLALHRWLH-WPRVYKAL
VPWFV MELNGHSKLYMKIDYEHNHGRKLLIEYPTFIIFTDCGIVYLALHRWLH-WPRVYR
APWFEL AEI RGYGVYVYDKLD-EYGYCFLFSSIALELLFSDFLIYWIHRALHHRWL-LYAPL
VSESME E-RGWTKCFASID-E-FGWIYLTVFVYIAIYLVLFVGYIYWMLREHLHDIKP-LYKYL
v p w f m -Ei-Gyskly-kid-E-hG-rkitie-atf-fFd-giY-aHrwLH-wp-YKAL

Transmembrane II His I

240 250 260 270 280 290
HKP HH---KWLVCTPFASHAFHPVDPGYFQSLSYHIYPMI-L-PLHKPSYI-LIFTFVNFWTV
HKP HH---KWLVCTPFASHAFHPVDPGYFQSLSYHIYPMI-L-PLHKPSYI-LIFTFVNFWTV
HKL HH---KWIWPTPFASHAFHYLDGYSOSSLPYHMFPEFF-PLNKKVYVYI-LIFTFVNFWTV
HAT HH---YKQNTLSPFAGLAHPVDPGILQAVP-HVIALFIVPTHTTHIGLLFMEA-IWTA
Hk p HH---Kwl vct Pfa shAHPv DPgyI Qsl -yH i ypl -i-Plh-k-syl -LFT f vnf Wt v

His II

300 310 320 330 340 350
MI HDGQHMSNN-PVVNGTACHTVHHLYFNYNYGQFTTLW-DRLGGSYRRP-EDSLFOPK
MI HDGQYLSNN-PAVNGTACHTVHHLYFNYNYGQFTTLW-DRLGGSYRRP-DDSLFDPK
MI HDGKYFSNN-AVVNGAAHAAHHMYFNYNYGQFTTLW-DRLGGSYRRP-DOBLFDAE
MI HDGCIH-GNIWPVM-GAGYHIIHTTYKHNHYGH-TIWMWMFGSLRDPPLLEED-DNK
MI HDgq---s-n-n-pvvng-ac-tt yH i yf ny NYGqft TI w-Drl ggg Sy Rr P-ds i l Dpk

Transmembrane III

360 370 380 390
dwf7-1 (W to Z) His III

400 410 420 430 440 450
LKMD KKVLEKQAF-ETAAYIQEVEGDDTDRVYNTD-KKKTN
LR- DAKETWDAQVK-EEVEHFIKEVEGDDNDRIYENDPNTKNN
LRNE KLOEQRIRFMEVYQY-TVEGKDLDRTYI-ASKKDN
DSEFAKAE -d-kk-e-q-r-et-yi-evegdd-dr-v-a-kk-n

FIG. 7

10 20 30 40

GAAGATCGATCAATCAATCATCAAACTCTGTGTGCCAC

50 60 70 80 90 100

41 ATGCATTACT ACTGTTGACT TGTTCATATA AGCTTAAAGTA AGATCAATCC GGGCAATCTT

110 120 130 140 150 160

101 CTTTCGTTT CCGGCACCGA TCTCCGTCGA TCTCCCATTC ACATGGCGGC GGATTAATGCT

170 180 190 200 210 220

161 TATCTGATC AGTTTGTCA CCAACCTCT TTTTACACCC GATCCTCTT CAGTCATCTT

Y L M Q F V D E T S F Y N R I V L S H L

230 240 250 260 270 280

221 TTGCCCCCGA ATCTATGGG ACCCTTACCT CATTTCCTCC AGACATGGCT CGGAAATTAC

L P A N L H E P L P H F L Q T H L R N Y

290 300 310 320 330 340

281 CTGGCCGGAA CCCTACTATA CTTCATCTCC GGTTCCCTCT GGTGCTTCTA CATCTATTAC

L A G T L L Y F I S G F L H C F Y I Y Y

350 360 370 380 390 400

341 CCTTAAATCA AGCTTACCT TCCCAAGGT CTGGATTTTC ACTTTTGTAT TCACTTATTC

L K I N V Y L P K

410 420 430 440 450 460

401 TTAACTCCCTT TCTATGTTAT CGATTTTCAT ATTAAAGGAA CGGGTTCTC TCGTGTACTC

470 480 490 500 510 520

461 TACAGTAAATT TGGATTTCAT CTGGATAGTT CATGTTTCAT TTTATTGATT ATTGTGCAAT

530 540 550 560 570 580

521 ATTCTCCATC TAAAGGATTG AACATTTAGT GGCTTATATA ACTTTTGTG CAACCATCA

590 600 610 620 630 640

581 GAACTGCTAC ATCTTTCAGT TTCAATTTC TACTTGCACT TTAACTCCAC TTAAATTCCTT

FIG. 8A

650 660 670 680 690 700
 641 TGTGAGTC ATTCCTACTT TTAGACACAA TTCTTTCT CCTCTCTGCA CACTCTGCT
 710 720 730 740 750 760
 701 TACTTGAAT TCTTTTTCG TCTGTTTGC TTCACTACAA ATTCCCTACAA TAAAGGCTAT
 770 780 790 800 810 820
 761 CCGTTTCAA ATGTTGTGG CATTGAGCC TATGCCATG TACACTCTTC TTCCACTGT
 830 840 850 860 870 880
 821 CTCCGAGCT ATGATTGAC GTGGTTCCAC CAAATGTTT CCTAGCATAG ACCGATTCCG
 890 900 910 920 930 940
 881 CTGGATTCTG TATTTGTTT ACATGGCAT CTATCTTGT TTGGTGTAGT TTGGTATTIR
 950 960 970 980 990 1000
 941 TTGGATCCAC AGGAGACCTTC ATGACATTAA CCCTCTCTAT AGCTATCTCC ATCCCACCC
 1010 1020 1030 1040
 1001 TCATATCTAC AGGAGAGAA ATACACTCTC TCCATTGCG G
 H I Y N K Q H T L S P F R

FIG. 8B

1050 1060 1070 1080
 1081 CTAGTGTT TTCAGTTTGT TCTTCTTTAG TTCTTGAA
 1090 1100 1110 1120 1130 1140
 1081 AGATTCGCTAG CATTAGTTT CTTACCAAGAA AAGACTTGT CAGCACCTGC TTGTACTCCA
 1150 1160 1170 1180 1190 1200
 1141 ATCACATTT TCCATTCCTT ATCCATTAAG TAACTCAGAA GGCTACATTT ATATAAATCT
 1218 1220 1230 1240 1250 1260
 1201 CAGCTGCATT ACTTCACATA TGTCAAGAGC ACTTCTCACT TAACTCAGCT TTAGATCTT
 1270 1280 1290 1300 1310 1320
 1261 CTGTTTCTCT TCTGGTCTCG GACTGATGG AATACCAAG AAGTTCTTT ATCTACTTCC
 1330 1340 1350 1360 1370 1380
 1321 CTGGAGTGTA TCTTGGTTAA TCCACCGATG TGACATCTAA TATTACTTGT AACTTCCTTA
 1390 1400 1410 1420 1430 1440
 1381 CCTTTTGT TACACCCCTT GCATTTCAAC CACTACACCG CATACTTCAG CCTGTACCCC
 GL R F H P V D G I L Q R V P
 1450 1460 1470 1480 1490 1500
 1441 ATGTGATAGC CCTGTTTATA GTCCCAATTTC ATTTCAACAC TCAATAGCT CTTTCTTCA
 H V I A L F I V P I H F T T H I G L L F
 1510 1520 1530 1540 1550 1560
 1501 TCGAACCGAT ATGGACCCCCG ARACTCCATG ACTGCATCCA TGGCCACATC TGGCCACATCA
 M E A I H T A N I H D C I H G H I W P V
 1570 1580 1590 1600 1610 1620
 1561 TGGCTCCACG ATACCATACG ATACACCAACA CGACATACACG CCATACATAT GGTCAATTATA
 M C R G Y H T I H H T T Y K H H Y G H Y

FIG. 8C

1621 1630 1640 1650 1660 1670 1680
 CCATATGAT CGATTGGATG TTTGGCTCTC TTAGGGATCC TCTCTTAGAA GAGATGACA
 T I W H D H M F G S L R D P L L E E D D
 1681 1690 1700 1710 1720 1730 1740
 ACAAAACAG CTTGAGAAA CCAGAGTAG AATGCCACT TGGTTTTGT TCTCTGTT
 N K D S F K K A E
 1741 1750 1760 1770 1780 1790 1800
 TGTCTTGCT TGTGTTGTT CAAACTTCA CCCTTCTTG TCTTTTCT TCTCTCTT
 1801 1810 1820 1830 1840 1850 1860
 ATTCACTGCT CTCTCTCAC CTTTCCATT ATATTCCTAC AARCATTTCC TGTCTAGTT
 1861 1870 1880 1890
 AARACATGTA AATCTTGTAT GATCTTTGCA

FIG. 8D

1 MAADNAYLMQ FVDETSFYNR IVLSHLLPAN LWEPLPHFLQ TWLRNYLAGT
51 LLYFISGFLW CFYIYYLKIN VYLPKDAIPT IKAMRLQMFV AMKAMPWYTL
101 LPTVSESMIE RGWTKCFASI DEFGWILYFV YIAIYLVFVE FGIVWMHREL
151 HDIKPLYKYL HATHHIYNKQ NTLSPFAGLA FHPVDGILQA VPHVIALFIV
201 PIHFTTHIGL LFMEAIWTAN IHDCIHGNIW PVMGAGYHTI HHTTYKHNYG
251 HYTIWMDWMF GSLRDPLLEE DDNKDSFKKA E

FIG. 9

10	30	50
GTTTGGTATTATTGGATGCACAGAGAGCTTCATGACATTAAGCCTCTATAAGTATCT CAAACCATAAAACCTACGTGTCTCGAAGTACTGTAATTGGAGAGATATTGATAGA		
70	90	110
CCATGCCACCCATCATATCTACAACAAGCAGAATACACTCTCTCCATTGCCGGTAAGTG GGTACGGTGGGTAGTATAGATGTTGTCGTTATGTGAGAGAGGTAAACGCCATTAC		
130	150	170
TTTCAGTTGTTCTTCTTAGTTCTGTAAAAGATTGGTAGCATTAGTTCTTACCA AAAAGTCAAACAAGAAGAAATCAAGAACATTCTAACCATCGTAAATCAAAGAATGGTC		
190	210	230
AAAAGACTTGTCAAGCAGCTGCTTGTACTCCAAATCACATTGCATTCCATTACCA TTTCTGAAACAGTCGTCGACGAACATGAGGTTAGTGTAAAACGTAAGGAATAGGTATT		
250	270	290
AGTAACCAGAAAGGCTAGAATTATATAATGTCAGCTGCATTACTCACATATGTCAGAG TCATTGGTCTTCGATCTAATATATTACAGTCGACGTAATGAAGTGTACAGTCTC		
310	330	350
AGACTTCTGACTTAACCAGAGTTAGATCTTGTGTTCTCTGGTCTCGGACTGATT TCTGAAGACTGAATTGGTCTCAAATCTAGAACACAAAGAGAACAGCCTGACTAA		
370	390	410
GGAAATGACGAGAAGTTCTTTATCTACTTCCCTGGAGTGTATCTGGTTAACCAAGGA CCTTACTGCTCTCAAGAAAATAGATGAAGGGACCTCACATAGAACCAATTAGGTTCT		
430	450	470
TGTGACATCTAAATATTACTTGTAACTTCCCTAACGTTTGTACAGGGCTTGCATTCA ACACTGTAGATTATAATGAACATTGAAGGAATGCAAAACAAATGTCCGAACGTAAGT		
490	510	530
CCCAGTAGACGGATACTTAAGGCTGTACCGCATGTGATAGCGCTGTTAGTGGCAATT GGGTCACTGCCCTATGAATTCCGACATGGCGTACACTATCGCGACAATATCACGGTTAA		
550	570	590
CATTTCACAACTCATATAGGTCTTGTACATGGAAGCGATATGGACGGCGAACATCCAT GTAAAGTGTGAGTATATCCAGAAAACAAGTACCTCGCTACCTGCCGTTGTAGGTA		

FIG. 10A

610 630 650
 GACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCAGGATACCATAACGATAACACCAC
 CTGACGTAGGTACCGTTGAGACCGGTCTTACCCACGTCTATGGTATGCTATGTGGTG

 670 690 710
 ACGACATACAAGCATAACTATGGTCATTATACCATATGGATGGATTGGATGTTGGCTCT
 TGCTGTATGTTCTGATTGATACCAAGTAATATGGTATACCTACCTAACCTACAAACCGAGA

 730 750 770
 CTTAGGGATCCTCTCTTAGAAGAAGATGACAACAAAGACAGCTCAAGAAAGCAGAGTGA
 GAATCCCTAGGAGAGAATCTTCTACTGTTGTTCTGTCGAAGTTCTTCGTCTCACT

 790 810 830
 GAATGCCCACTGGGTTTGTCTTCTGTTCTGTCTGTTGTTGTTGTTCAAAGTT
 CTTACGGGTGAACCCAAAACAAGAACAGACAAAACAGAACACAACAACAAGTTCAAAG

 850 870 890
 AGCCTTCTTGTCTTTCTTCTTCTTCTTATTGATGTGTCCTCTCAACCTTCCAAT
 TCGGAAAGAACAAAGAAAAGAAGAACAGAACAGAACAGAGAGTTGGAAAGGTAA

 910 930 950
 TATATTGTTACAAACATTGCTGCTAGTTAAAACATGTAATGTTGATGATCTTGC
 ATATAACAATGTTGTAACGACAGATCAAATTGTCATTTACAAACTACTAGAACG

 970 990 1010
 AAGACTCCATTGGTTAAGGTAACCTGAACTCATAGATTGTCATTGGTATT
 TTCTGAGGTAAAACAAATTCCATTGAACTTAGAGTATCTAACAGCTAACACCATAA

 1030 1050 1070
 TCCATTTCAAGGTACGGTTCTGTAGACTGTAGTCTGCTGACCAGTCGGCTTAACCACC
 AGGTAAAAGTCCATGCCAAGACATCTGACATCAGAACGACTGGTCAGGCCGAATTGGTGG

 1090 1110 1130
 CCAAATTCAAGATCTC_cCAATCAAAATGCTGGCTGGCCCAATATATAGATGGGCCA
 GGTTAAAGTTCTAGAGT_gGTTAGTTACGACCGACCGGGTTATATATCTACCCGGT

 1150 1170 1190
 GTTAATCCGCTAGCTTACTCTTAGACCTACCTAGACAGTTAGACACCTGCTAATTA
 CAATTAGGCAGATCGAAATGAGAAATCTGGATGGAATCTGTCATCTGTGGACGATTAAT

FIG. 10B

1210	1230	1250
ATGAGTTCCCTTTCTTGTTCAGCAAGTTACCTGTGTTACTGAGAGTTGAGTTAATGG TACTCAAAGAAAAAGAACAGTCGTTCAATGGACACAATGAACACTCAACTCAATTACC		
1270	1290	1310
TAGTAAACGCAATTAAACCTTATAAGTTAACGTATTCAACGAATGACCCAGAGACTT ATCATTGCGTTAAATTGGGAATATTCAAATTAGCATAAGTTGCTTACTGGTCTCTGAA		
1330	1350	1370
TAAATAAATCCATCGTAACCCTCCACTTCAAAATTCTTTAAAAAGTAGCAAATCATT ATTTATTAGGTAGCATGGGAGGTGAAGTTAAGAAAAATTTCATCGTTAGTAAA		
1390	1410	1430
AAATATTGTAAGTTGCTCATTCAAACGAAATTGTAGCTACAGATCTCAAAGCTCCTCGTT TTTATAACATTCAAACGAAGTAAGCTTAACATCGATGTCTAGAGTTGAGGAGGACAA		
1450	1470	1490
GGCCATATCTCTCTAAACAAACGATAGTAACACTTGACCACAGTTGACTTCCTCGCG CCGGTATAGAGAGAGATTGTTGCGTATCATTGTGAACGTGTCAAACTGAAGAGCCGC		
1510	1530	1550
GTTTCATGGCGCGACTATGGCAGATTATAATGATCAGATCGTCAATGAGACCTCTT CAAAGTACCGCCGCTGATACCGTCTAAATTACTAGTCTAGCAGTTACTCTGGAGAAAAA M A A T M A D Y N D Q I V N E T S F Y		
1570	1590	1610
ACAACCGAAtGGTTCTGAGTCACCTTTGCCGgTGAATCTATGGAACCTTACCACTT TGTGGCTTACAAGACTCAGTGGAAAACGGCcACTTAGATAACCTGGAAATGGtGTAA N R M V L S H L L P V N L W E P L P H F		
1630	1650	1670
TCCTCCAGACATGGCTCCGAACTACCTCGCCGAAACATACTCTACTTCATCTCCGGCT AGGAGGTCTGTACCGAGGCCCTGATGGAGCCGCTTGTATGAGATGAAGTAGAGGCCGA L Q T W L R N Y L A G N I L Y F I S G F		
1690	1710	1730
TCCTCTGGTGCTTACATCTATTACCTAAACTCAACGTTACGTCCCCAAAGGTTACT AGGAGACCACGAAGATGTAGATAATGGAATTGAGTTGCAAATGCAGGGTTCCAATGA L W C F Y I Y Y L K L N V Y V P K		

FIG. 10C

1750	1770	1790
TTTTCAATTGATGTTCTGTTGAAACCTTCTTTGTTGATTCCCTCGATTGTATC AAAAAGTTAAAGCTACAAGACAAAACTTGAAAGAAAACAACTAAGGAAGCTAACATAG		
1810	1830	1850
GCCTGATAGATTGTGTTACGTTAACCTTTCTTACTGTTACTTCAGTTCTGTC CGGACTATCTAACACAATATGCAATTGGAAAAAGAATGACAATGAAAGTCAAGAACAG		
1870	1890	1910
TTCTACTTCTCATTTAATTAGTTAAAGTTAATATTTTGGCTAATCCACATTTTA AAGATGAAGAGTAAATTAAATCAAATTATAAAAACGATTAGGTGTAAAAAT		
1930	1950	1970
AGTTGAATCTTCCATGAAATTGAGCTAAAATATACCATGAAATTGAAATTGTGGTTC TCAACTTAGAAGGTACTTAAACTCGAGTTTATATGGTACTTTAACACACCAAG		
1990	2010	2030
TTAGTTCTATTCTTGCTGGTTCTTCTATTTTGTGGTTAGAATCCATTCCTACGAGA AATCAAGATAAAGAACGAAACCAAGAAGATAAAACCCAATCTTAGTAAGGATGCTCT		
E S I P T R		
2050	2070	2090
AAGGCAATGCTTGC _A ATATACGTGGCAATGAAGGCTATGCCCTGGTACACTCTTCTT TTCCGTTACGAAACGTTATATGCACCGTTACTCCGATA _C GGAACCAATGTGAGAAGAA		
K A M L L Q I Y V A M K A M P W Y T L L		
2110	2130	2150
CCAGCTGTCTGAGTATATGATCGAGCATGGTGGACCAATGTTACTCTACACTTGAC GGTCGACAGAGACTCATATACTAGCTCGTACCAACCTGGTTACAATGAGATGTGA _C GT		
P A V S E Y M I E H G W T K C Y S T L D		
2170	2190	2210
CATTCAACTGGTTCCTGTTCTCTACATAGCTCTATCTTGT _T TAGTTGAGTT GTAAAGTTGACCAAGGAGACAAAGGAGATGTATCGAGAGATAGAACAAATCAACTCAA _a		
H F N W F L C F L Y I A L Y L V L V E F		
2230	2250	2270
ATGATTTATTGGGTTACAAAGAGCTTCATGACATTAAATTCTCTATAAGCATCTCCAT TACTAAATAACCCAAGTGTTCGAA _T ACTGTAATTAAAGAGATATT _C GTAGAGGTA		
M I Y W V H K E L H D I K F L Y K H L H		

FIG. 10D

2290	2310	2330
<pre> GCTACCCATCATATGTACAACAAGCAAAACACACTCTCTCCATTGCCGGTATGTCAAAG CGATGGGTAGTATACATGTTGTTGTGAGAGAGGTAAACGCCATACAGTTTC A T H H M Y N K Q N T L S P F A </pre>		
2350	2370	2390
<pre> CTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGGTACTTCTTACTTGATGT GATATACAAGAGTTAGATTTAACATAGTTACCACTGAAGAAATGAACACTACA </pre>		
2410	2430	2450
<pre> TTTCGGGTTTCAGGGCTCGCATTCCATCCGCTGGACGGGATACTTCAGGCTATACCGC AAAAGCCAAAAGTCCCAGCGTAAGGTAGGCGACCTGCCCTATGAAGTCCGATATGGCG G L A F H P L D G I L Q A I P H </pre>		
2470	2490	2510
<pre> ACGTGATAGCGCTGTTATAGTGCCATTCTCATCTCATAACACATCTGAGTCTTTGTTT TGCACATCGCGACAAATATCACGGCTAAGTAGAGTATTGTTAGACTCAGAAAACAAAA V I A L F I V P I H L I T H L S L L F L </pre>		
2530	2550	2570
<pre> TGGAAAGGGATATGGACAGCAAGCATCCATGATTGCATACATGGAACATCTGGCCTATAA ACCTTCCCTATACCTGTCTCGTAGGTACTAACGTATGTACCTTGTAGACCGGATAATT E G I W T A S I H D C I H G N I W P I M </pre>		
2590	2610	2630
<pre> TGGGTGCAGGATACCATACCATACACCATAACACATACAAGCATAACTATGGTCATTATA ACCCACGCTCTATGGTATGGTATGGTATGGTATGTTGTATTGATACCACTAATAT G A G Y H T I H H T T Y K H N Y G H Y T </pre>		
2650	2670	2690
<pre> CCATATGGATGGACTGGATTTGGCTCTCTTATGGTCCCTTAGCAGAAAAACACAGTT GGTATACCTACCTGACCTACAAACCGAGAGAATACCAAGGAATCGCTTTCTGTCAA I W M D W M F G S L M V P L A E K D S F </pre>		
2710	2730	2750
<pre> TCAAGGAGAAAGAAAAGTGGAGAATGTTCAATGCTCACATGTATTCTCATATGTTGCTCT AGTCCCTCTTCTTCACTCTAACAGTTACCGAGTGTACATAAGAAGTATACAACGAGA K E K E K * </pre>		
2770	2790	2810
<pre> TCTCGTACTCTTATTAAAACCTTCTAATCACTTGGTGGAAATTAAAACATGACTGCA AGAGCACTGAGAATAATTGGAAAGATTAGTGAAACCACCTTAATTGTACTGACGT </pre>		

FIG. 10E

2830 2850 2870
TAATTTGATGCAAAGTTTCAGACTTTATTGCTAAAAATCTCTGATGATTATTAACCTCA
ATTAAACTACGTTCAAAGTCTGAAAATAACGATTAGAGACTACTAATAATTGGAGT
2890 2910
ATTATATAATTGcTGGATGAAGAGTTCAAATTGGACTAAATCTG
TAATATATTAACgACCTACTTCTCAAGTTAACCTGATTAGAC

FIG. 10F

1 maatmadynd qivnetsfyn rmvlshllpv nlwepiphfl qtwlrnylag
51 nilyfisgfl wcfyiyylkl nvyvpkesip trkamllqiy vamkampwyt
101 llpavseymi ehwgwtkcyst ldhfnwflcf lyialylvlv efmiywhke
151 lhdikflykh lhathhmynk qntlspfagl afhpldgilq aiphvialfi
201 vpihlithls llflegiwta sihdcihgni wpimgagyht ihhttykhny
251 ghytiwmdwm fgslmvplae kdsfkekek

FIG. 11